

## **AMENDMENTS TO THE CLAIMS**

This listing of claims will replace all prior versions, and listings, of claims in the application:

### **LISTING OF CLAIMS:**

1. – 58. (Cancelled).

59. (Previously presented) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with a nucleic acid encoding an amino acid sequence that is greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1, SEQ ID NO.: 1.

60. (Previously presented) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with an antibody that specifically binds to a protein that is greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1, SEQ ID NO.: 1.

61. (Previously presented) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with a first group of one or more nucleic acids that hybridize under stringent conditions to a second group of one or more nucleic acids, that encodes a protein, or fragment thereof, consisting of sequence that is greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1, SEQ ID NO.: 1.

62. (Previously presented) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with one or more nucleic acids that hybridize under stringent conditions to the genome or antigenome of the virus isolate deposited as I-2614 with CNCM, Paris.

63. (Previously presented) The method of claim 59, wherein the amino acid is:  
SEQ ID No.: 1.

64. (Cancelled).

65. (Cancelled).

66. (Previously presented) The method of claim 60, wherein the protein consists of an amino acid sequence of SEQ ID No.: 1.

67. (Previously presented) The method of claim 66, wherein the method further comprises an immune fluorescence assay.

68. (Previously presented) A method for detecting an antibody against human metapneumovirus in a sample, wherein the method comprises contacting the sample with a protein comprising the amino acid sequence of: SEQ ID No.: 1.

69. (Previously presented) The method of claim 59 or 62, wherein the nucleic acid is at least 90% identical to SEQ ID No.: 1.

70. (New) The method of claim 62, wherein the one or more nucleic acids are at least 90% homologous to the genome or antigenome of the virus isolate deposited as I-2614 with CNCM, Paris.